Online Proceedings

Poster Session 1

Commons West, Easel 2

11:00 AM to 1:00 PM

Household Air Pollution and its Repercussions on Health in Developing Countries

Federico (Freddie) Pastoris, Junior, Global Studies (Bothell)
Mentor: Benjamin Gardner, Interdisciplinary Arts & Sciences

Almost 3 billion people, coming mostly from low-middle income countries, still rely on unprocessed solid fuels (wood, dung, crop, waste, kerosene, charcoal) as their main source of energy to fulfill daily needs, such as cooking, heating and lighting. The prolonged exposure to this form of pollution is strongly correlated to pneumonia and acute respiratory infections (ARI) in children and to chronic obstructive pulmonary disease (COPD) in women. I began this project by analyzing the correlation between these respiratory infections and high exposure levels to particulate matter and CO present in the heavy smokes produced by wood-powered cookstoves. I then conducted a preliminary field study in Granada, Nicaragua, to evaluate the effectiveness of ongoing projects and to examine the elements involved in adoption levels of alternative cookstoves. Speaking fluent Spanish allowed me to collaborate with a Nicaraguan NGO that manufactures, sells and distributes clean cookstoves. Through this organization I approached local community members from a rural area near Granada and conducted both participant and nonparticipant observations of local cooking practices and fuel uses. These observations were supported by informal semi-structured interviews about costs, logistics and household financial management dynamics involved in fuel purchasing (wood). I also analyzed the implementation of wood for cooking practices and the related cultural elements. As an example, the long-standing cultural tradition of cooking on a big open-air fire using large quantities of wood correlates with prestige and wealth within the community. These early findings have informed a second study that I will carry out in July and August 2017 in Nicaragua, which addresses more specific questions about the cultural appropriateness of different alternative cookstoves and the related adoption levels.

Poster Session 2

MGH 241, Easel 128

1:00 PM to 2:30 PM

Induction of Ureteric Bud Progenitor Cells from Human Pluripotent Stem Cells

Laura Victoria Islas, Sophomore, Pre Engineering
Mary Gates Scholar
Mentor: Benjamin Freedman, Medicine/Nephrology

Currently, the only two treatments available to people with chronic kidney disease are organ transplants and dialysis. With such a high demand for kidneys, regenerative medicine is needed to create new therapies. Human pluripotent stem cells (hPSCs) can be used to generate immunocompatible tissues on-demand, which can be used to study human disease processes or potentially transplanted back into the original patient as a tissue replacement therapy. New protocols allow the differentiation of pluripotent stem cells into small, kidney-like organoids that contain the major proximal structures of the nephron, the functional subunit of the kidney. These organoids include podocytes, proximal tubules, distal tubules, and endothelial cells, but they lack a collecting duct system, a crucial component of the kidney. To address this need, we have developed a protocol to differentiate hPSCs into ureteric bud (UB) cells, which are the precursors of collecting duct cells. Undifferentiated hPSCs were treated with a growth factor, glial cell line-derived neurotropic factor (GDNF), that signals the outgrowth of the UB in the human kidney, and a differentiation factor, CHIR 99021, at different concentrations. Immunofluorescence was used to characterize the resulting cells, which were stained with Dolichos biflorus agglutinin (DBA), a collecting duct marker, DAPI, a DNA marker, and GATA 4, a transcription factor that is important for kidney development. We found that both DBA and GATA 4 were co-expressed together in isolated patches of cells under one of the conditions tested. This staining pattern suggested that these were UB cells. This is the first time UB cells have been differentiated from hPSCs. The development of this differentiation protocol will lead to the growth of the collecting duct system in the kidney organoids, which will optimize them for kidney disease modeling, high-throughput drug screening, and regenerative medicine approaches to reduce the need for kidney transplants.

POSTER SESSION 2

MGH 241, Easel 129

1:00 PM to 2:30 PM

Using Induced Pluripotent Stem Cells to Change Urine into Kidney Organoids

Kezia Philip, Senior, Bioengineering
Mary Gates Scholar
Mentor: Benjamin Freedman, Medicine/Nephrology
Mentor: Nelly Cruz, Medicine

The goal of this research is the generation of induced pluripotent stem (iPS) cells and derived kidney organoids from urinary cells. iPS cells are somatic cells reprogrammed to an undifferentiated state, making them an exciting advancement in regenerative medicine as they could model an in-vitro progression of many disorders and show great promise for replacing or repairing tissue damaged due to disease or injury. To generate new kidney tissues, adult somatic cells were isolated from a patient's urine sample. This method of sample collection is advantageous over the traditional skin biopsy because it does not require a physician and is easier for the patient to supply. This protocol was further optimized to accommodate remotely collected urine samples, showing the ability to isolate somatic cells from patients located across the globe. We successfully isolated somatic cells with various morphologies, ranging from epithelial to mesenchymal-like cells, from 25 different patients. By introducing into these cells RNA encoding four specific transcription factors, a safer alternative to introducing DNA as it eliminates the risk of inserting a mutation into the patient's genome, we successfully reprogrammed urinary cells of an international patient with autosomal recessive polycystic kidney disease into iPS cells. These iPS cells were further differentiated into kidney organoids, which have the capacity to become a powerful tool in improving current therapies for kidney disease as an in-vitro model. Thus, for the first time, we have generated patient-specific kidney tissue from a urine sample. This will increase our understanding of the disease and improve current methods for the screening of investigational therapeutics. The ability to create new kidney tissues in the lab also raises the possibility of transplanting these tissues back into their original patients, where they could potentially function without the need for immunosuppression.

SESSION 2E

ADVANCED TECHNOLOGIES FOR HEALTHCARE AND OTHER APPLICATIONS

Session Moderator: Daniel Kirschen, Electrical Engineering

MGH 238

3:30 PM to 5:15 PM

* Note: Titles in order of presentation.

The Impact of Blade Mounting Geometry on Cross-Flow Turbine Performance

Noah E (Noah) Johnson, Senior, Mechanical Engineering
UW Honors Program
Mentor: Brian Polagye, Mechanical Engineering
Mentor: Benjamin Strom, Mechanical Engineering

Cross-flow turbines are a promising approach for extracting renewable energy from tidal and river channels. These turbines consist of a set of blades rotating about an axis perpendicular to the water flow direction. While blade mounting geometry has implications for parasitic drag, lift-induced drag, and blade lift generation, which strongly influence turbine performance, little research has been published on this topic. The impact of blade mounting geometry on turbine performance was evaluated by comparing the power conversion efficiency of ten two-bladed turbines with varying mounting geometries in a recirculating water flume. Each turbine was also tested without blades to evaluate interactions between blades and mounting geometry. A servomotor rotated the test turbine at constant angular velocity and two six-axis load cells were used to measure the torque produced by the turbine rotor. Six tests were performed with connecting struts at each end of the blades. Cross sectional geometry (rectangular, rounded, and foil) and thickness were varied (chord length held equal to the blade). Three tests were also performed with solid disks of varying radii mounted to each end of the blade. Finally, one test was performed with a single foil strut mounted at the center of blade span. Complete performance curves at four Reynolds numbers were generated for each mounting geometry by varying the free stream velocity. At the highest Reynolds number, the thin foil strut performed with greatest efficiency, followed by the thin rounded strut and thick foil strut. The smallest disk, thin rectangular strut, and thick rounded strut performed similarly. Strut and disk drag was analytically modeled and compared with experimental data to characterize power loss from each mounting geometry. These results offer insight into cross-flow turbine design for optimal efficiency and encourage investigation of additional mounting geometries such as winglets or curved mounting interfaces.

Poster Session 3

Balcony, Easel 90

2:30 PM to 4:00 PM

Using Thermal Infrared Remote Sensing to Identify Effects of Beaver Dams on Stream Temperature

Alishia Orloff, Sophomore, Environmental Science & Resource Management
Mentor: Benjamin Dittbrenner
Mentor: Joshua Lawler, School of Environmental and Forest Sciences

Beavers create complex modifications to the physical and biological components of stream ecosystems through their creation of dams and wetland complexes. Beaver impoundments alter the movement of surface and subsurface waters through riparian systems, which substantially affects biotic and abiotic ecosystem processes that together make up habitats for different species. Although there is general agreement that beaver impoundments modify stream temperature, there has been very little focus on their effect at larger spatial scales. In prior research, traditional temperature assessment methods have failed to capture the full spatial breadth of riverine systems. The use of thermal infrared remote sensing (TIR) is an effective tool for measuring surface stream temperature variability at landscape scales. To better understand the role of beavers in the regulation of stream temperature, we evaluated TIR imagery collected within the Snoqualmie and Stillaguamish River basins in Washington State. Our objective was to identify whether TIR imagery could be used to identify areas where beaver dam complexes have measurable effects in decreasing downstream water temperature due to the upwelling of groundwater. We used an intrinsic potential beaver habitat model to identify areas within the TIR flight paths where beavers were likely present and surveyed these areas to confirm presence of beaver wetland complexes. We compared upstream and downstream surface temperature, thermal complexity, and heterogeneity within these areas using a suite of spatial statistics. Our results have the potential to demonstrate that the use of TIR is a novel approach for monitoring the effects of beaver on riparian systems. Its use provides for assessments at scales and breadth not previously possible using traditional approaches.

Poster Session 3

MGH 206, Easel 165

2:30 PM to 4:00 PM

Effects of Viral Mutations in the Evolution of Thermotolerance

Erin Mc Clure, Senior, Biology (General)
Mary Gates Scholar, UW Honors Program
Mentor: Benjamin Kerr, Biology
Mentor: Sonia Singhal, Biology

Mutations have a large range of effects on an organism's observable characteristics, from neutral (no effect) to deleterious (lower an organism's fitness) to beneficial (increase an organism's fitness). I engineered three mutations into the virus phi-6 and evaluated their effects on viral thermotolerance and growth. Because these mutations were found in a population that had experienced high temperature heat shocks, I hypothesized that the mutant viruses would have a higher thermotolerance than the ancestral virus. To test the thermotolerance of these mutations, I heat shocked bacteria-free lysates of mutant virus and ancestral virus at various temperatures and then calculated the percent survival of the lysate at each temperature. The mutants were also evaluated for their fitness through growth competitions with a common competitor. I found that only one mutation conferred a higher thermotolerance than the ancestor. However, fitness competitions showed that all mutations and combinations of mutations did increase viral growth. This suggested that additional selective pressures may have been present in the evolution experiment. Specifically, the viruses had been grown at low temperatures between heat shocks, which may have resulted in the evolution of higher growth rates, even at the cost of thermotolerance. My research shows that all selective pressures must be taken into consideration when studying evolutionary trajectories. We cannot accurately predict how organisms will evolve in response to one selective pressure such as increased environmental heat without taking in to account the other selective pressures they experience.

Poster Session 3

Balcony, Easel 107

2:30 PM to 4:00 PM

Loss of the Type VI Secretion System from a Human Gut Bacterium via Experimental Evolution

Georgie Lynn (Georgie) Mullen, Sophomore, Pre-Health Sciences
Mentor: Joseph Mougous, Microbiology
Mentor: Benjamin Ross, Microbiology

Human-associated bacteria are important for human health, but little is known about how these bacteria interact with each other. *Bacteroides fragilis (B. fragilis)* is a Gram-negative bacteria that is found in the human gut and assists in nutrition. *B. fragilis* genomes encode the type VI secretion system (T6SS), a needle-like structure that transports toxins into nearby competitor cells. T6SS is used to gain advantage over competitors, yet our lab has observed that *B. fragilis* strains in adults are four times more likely to lack T6SS than strains in infants, suggesting *B. fragilis* may lose this mechanism over time. Why would T6SS be lost if it is used to gain an advantage over competitors? I hypothesize that *B. fragilis* inactivates T6SS because it is no longer required. To test this, I passaged *B. fragilis* strains with T6SS under competition conditions in which the recipient is either susceptible or immune to the effects of T6SS-delivered toxins. I predicted that recipients with immunity will cause *B. fragilis* to inactivate its T6SS mechanism, while predicting recipients that are susceptible to be killed off by the toxins delivered via T6SS in *B. fragilis*. Competitions proceeded for 24 hours, followed with the selection of the donor strain by addition of antibiotics. After selection of donor strains, each were archived in glycerol for evolutionary documentation. Subsequent passages were commenced with newly selected donors. Every 5 generations, competitions proceeded to evaluate competitive fitness of T6SS; whether or not *B. fragilis* has inactivated its T6SS. Whole genome sequencing revealed the mechanism by which T6SS was inactivated at the level of DNA mutations. By using experimental evolution to study interbacterial interactions within the human gut, we will have a better understanding of the long-term dynamics of the human microbiome and its role in influencing human health.

POSTER SESSION 3

MGH 206, Easel 166

2:30 PM to 4:00 PM

Compensatory Mutations Increase the Maintenance of Antibiotic Resistant Plasmids in Bacterial Hosts

Jessica Lange, Senior, Biology
Mary Gates Scholar
Mentor: Benjamin Kerr, Biology
Mentor: Hannah Jordt, Biology

Plasmids are small circular pieces of DNA that replicate separately from the chromosome. Plasmids often contain antibiotic resistance genes that allow their host bacteria to grow in environments containing that antibiotic. They can be transmitted both vertically during cell division, and horizontally via conjugation to new bacterial hosts, and thus spread antibiotic resistance through populations. Plasmids are often costly to their bacterial hosts when not in the presence of antibiotics, but the coevolution of a bacteria and plasmid can reduce these costs through compensatory mutations. Typically a reduction or an amelioration of plasmid cost is seen during plasmid/host coevolution, but not a fitness benefit. However, preliminary data has shown evidence of a fitness advantage to containing a plasmid for the bacterial host Pseudomonas sp. nov. H2 after it was evolved with the plasmid RP4. In this project, I determined whether the fitness benefit seen in the aforementioned plasmid/host pair also occurs in three other bacterial species with different plasmid types. For each of these pairs the plasmids initially conferred a cost to the host. We hypothesized that compensatory mutations (on either the host chromosome or the plasmid) would result in the reduction, amelioration or reversal of the initial high cost of maintaining a plasmid for all three pairs. To test this, we evolved three plasmid/host pairs in antibiotic-containing media for several hundred generations, selecting for antibiotic resistance genes on the plasmids. We ran competitions between an evolved host/evolved plasmid pair and an evolved host with the plasmid removed, to determine whether there remained a cost to containing a plasmid, or whether that cost has been reduced, ameliorated, or reversed. Our experiments will help explain why plasmid-conferred antibiotic resistance persists in bacterial populations.

POSTER SESSION 4

Commons West, Easel 8

4:00 PM to 6:00 PM

Evolution Outliers: Characterizing Emission Line Stars

Aislynn Wallach, Junior, Physics: Comprehensive Physics, Astronomy
NASA Space Grant Scholar
Mentor: Benjamin Williams, Astronomy

Our goal is to quantify the fraction of H-α emitting B stars in M31. A small subset of massive stars emits strongly in H-α, which indicates the presence of hotter gas than is typically associated with such stars. These stars' line emission may be related to stellar rotation, but it is unclear what causes the rotation or if there are other possible causes for the line emission. In order to shed light on this problem, we've begun a project to identify a homogeneous sample of these stars in M31. Our data are comprised of imaging from six fields in M31. Using resolved photometry of over two million stars, we have found 50 candidates. Using a ratio of these candidates to ordinary stars of the same temperature that are not emitting in the H-α, we can put observational constraints on models of the formation of stars in this mass range, as any viable model must be able to reproduce the observational statistics of these rare stars. Therefore, despite their rarity, they provide a key diagnostic of stellar evolution models fundamental to many fields of astrophysics.

POSTER SESSION 4

Commons West, Easel 7

4:00 PM to 6:00 PM

High-Resolution Multi-Wavelength Examination of a Supernova Remnant in the Nearby Spiral Galaxy NGC 300

Jacob Alexander Gross, Senior, Computer Science, Physics: Comprehensive Physics
Mary Gates Scholar
Mentor: Benjamin Williams, Astronomy

Supernovae enrich the interstellar medium, allowing it to create fascinating and exciting objects such as stars, planets, and people. However, supernovae are difficult to study because, most of the time, we do not observe these supernovae directly, since the whole event can occur in a very short time. Fortunately, they leave behind bright remnants that can give us information about the supernova and even the stars that existed before. We have observed one such supernova remnant in the nearby spiral galaxy NGC 300, which is approximately three million light years away from Earth. We have acquired multi-wavelength data of this source from *Chandra X-ray Observatory*, *XMM-Newton X-ray Observatory*, and *Hubble Space Telescope*. Using this variety of telescopes, we can understand how this supernova remnant behaves in both the x-ray and optical energy bands which gives us a more complete picture of our source. From our *Hubble* data, we gain detailed measurements of the size and shape of the source. From our *Chandra* and *XMM-Newton* data, we can shed light on the properties of this supernova remnant by performing a spectral analysis on the x-ray data. This spectral analysis gives us information about the temperature and metallicity of the source, as well as the density of the surrounding gas. With these quantities, we can better understand this supernova remnant and supernova remnants like it which, in turn, let us better understand the life of the star that created this source.